RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/534,894

Source: PCT

Date Processed by STIC: 5-25-05

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PCT

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RAW SEQUENCE LISTING                    DATE: 05/25/2005
PATENT APPLICATION:  US/10/534,894      TIME: 11:40:08

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Output Set: N:\CRF4\05252005\J534894.raw
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      3 <110> APPLICANT: SHANGHAI INSTITUTES FOR BIOLOGICAL SCIENCES, CAS
      5 <120> TITLE OF INVENTION: METHOD OF DIAGNOSING AND TREATING BALDNESS USING HUMAN AND
MOUSE RHOR
      6       GENE AND CODED PRODUCT THEREOF
      8 <130> FILE REFERENCE: 026816 pc
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/534,894
C--> 10 <141> CURRENT FILING DATE: 2005-05-13
     10 <150> PRIOR APPLICATION NUMBER: CN 02145353.9
     11 <151> PRIOR FILING DATE: 2002-11-13
     13 <160> NUMBER OF SEQ ID NOS: 14
     15 <170> SOFTWARE: PatentIn version 3.1
     17 <210> SEQ ID NO: 1
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     19 <212> TYPE: DNA
     20 <213> ORGANISM: Mus musculus
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     23 <221> NAME/KEY: CDS
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     33 agc cgc ctg cag agc cgg aag cca ccc aac ctc tcc atc acc atc ccg        96
     34 Ser Arg Leu Gln Ser Arg Lys Pro Pro Asn Leu Ser Ile Thr Ile Pro
     35              20                  25                  30
     37 cca cca gag agc cag gcc ccc ggc gag cag gat agc atg ctt cct gag       144
     38 Pro Pro Glu Ser Gln Ala Pro Gly Glu Gln Asp Ser Met Leu Pro Glu
     39              35                  40                  45
     41 agg cgc aag aac cca gcc tac ctg aag agt gtc agc cta cag gag ccc       192
     42 Arg Arg Lys Asn Pro Ala Tyr Leu Lys Ser Val Ser Leu Gln Glu Pro
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     45 cgg gga cga tgg cag gag ggc gca gag aag cgc ccc ggc ttc cgc cgc       240
     46 Arg Gly Arg Trp Gln Glu Gly Ala Glu Lys Arg Pro Gly Phe Arg Arg
     47 65                  70                  75                  80
     49 cag gcc tcc ctg tcc cag agc atc cgc aag agc aca gcc cag tgg ttt       288
     50 Gln Ala Ser Leu Ser Gln Ser Ile Arg Lys Ser Thr Ala Gln Trp Phe
     51              85                  90                  95
     53 ggg gtc agc ggc gac tgg gag ggc aag cga caa aac tgg cat cgt cgc       336
     54 Gly Val Ser Gly Asp Trp Glu Gly Lys Arg Gln Asn Trp His Arg Arg
     55              100                 105                 110
     57 agc ctg cac cac tgc agc gtg cac tat ggc cgc ctc aag gcc tcg tgc       384
     58 Ser Leu His His Cys Ser Val His Tyr Gly Arg Leu Lys Ala Ser Cys
     59              115                 120                 125
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 62 Gln Arg Glu Leu Glu Leu Pro Ser Gln Glu Val Pro Ser Phe Gln Gly
 63     130                 135                 140
 65 act gag tct cca aaa ccg tgc aag atg ccc aag att gtg gat cca ctg       480
 66 Thr Glu Ser Pro Lys Pro Cys Lys Met Pro Lys Ile Val Asp Pro Leu
 67 145                 150                 155                 160
 69 gct cgg ggt agg gcc ttc cgc cat cca gat gag gtg gac cgg cct cac       528
 70 Ala Arg Gly Arg Ala Phe Arg His Pro Asp Glu Val Asp Arg Pro His
 71                 165                 170                 175
 73 gct gcc cac cca cct ctg act cca ggg gtc ctg tct ctc aca tcc ttc       576
 74 Ala Ala His Pro Pro Leu Thr Pro Gly Val Leu Ser Leu Thr Ser Phe
 75             180                 185                 190
 77 acc agt gtc cgc tct ggc tac tcc cat ctg ccc cgc cgc aag agg ata       624
 78 Thr Ser Val Arg Ser Gly Tyr Ser His Leu Pro Arg Arg Lys Arg Ile
 79         195                 200                 205
 81 tct gtt gcc cat atg agc ttt cag gca gcc gcc gcc ctc ctc aag ggg       672
 82 Ser Val Ala His Met Ser Phe Gln Ala Ala Ala Ala Leu Leu Lys Gly
 83     210                 215                 220
 85 cgt tcc gtg cta gat gcg act ggg cag cgg tgc cgg cat gtc aaa cgc       720
 86 Arg Ser Val Leu Asp Ala Thr Gly Gln Arg Cys Arg His Val Lys Arg
 87 225                 230                 235                 240
 89 agc ttc gct tac ccc agc ttc ctg gag gag gat gct gtc gat gga gct       768
 90 Ser Phe Ala Tyr Pro Ser Phe Leu Glu Glu Asp Ala Val Asp Gly Ala
 91                 245                 250                 255
 93 gac acc ttc gac tcc tcc ttt ttt agt aag gaa gaa atg agc tcc atg       816
 94 Asp Thr Phe Asp Ser Ser Phe Phe Ser Lys Glu Glu Met Ser Ser Met
 95             260                 265                 270
 97 cct gac gat gtc ttt gag tcc ccc cca ctc tct gcc agc tac ttc cga       864
 98 Pro Asp Asp Val Phe Glu Ser Pro Pro Leu Ser Ala Ser Tyr Phe Arg
 99         275                 280                 285
101 ggt gtc cca cac tct gcc tcc ccg gtc tcc ccg gat gga gtg cac atc       912
102 Gly Val Pro His Ser Ala Ser Pro Val Ser Pro Asp Gly Val His Ile
103     290                 295                 300
105 ccg cta aaa gaa tac agc ggt ggc cga gcc ctg ggt ccc ggg acc cag      960
106 Pro Leu Lys Glu Tyr Ser Gly Gly Arg Ala Leu Gly Pro Gly Thr Gln
107 305                 310                 315                 320
109 cgt ggc aaa cgc att gcc tcc aaa gta aag cac ttt gca ttt gac cgg     1008
110 Arg Gly Lys Arg Ile Ala Ser Lys Val Lys His Phe Ala Phe Asp Arg
111                 325                 330                 335
113 aag aag agg cac tac ggc ctg ggt gtc gtg ggt aac tgg ctc aac cga     1056
114 Lys Lys Arg His Tyr Gly Leu Gly Val Val Gly Asn Trp Leu Asn Arg
115             340                 345                 350
117 agc tat cga cgc agc atc agc agc acc gtg cag cgg cag ctg gag agc     1104
118 Ser Tyr Arg Arg Ser Ile Ser Ser Thr Val Gln Arg Gln Leu Glu Ser
119         355                 360                 365
121 ttc gat agc cac cgg ccc tac ttc acc tac tgg ctg acg ttc gtt cac     1152
122 Phe Asp Ser His Arg Pro Tyr Phe Thr Tyr Trp Leu Thr Phe Val His
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130 Gly Phe Ala Gln His Val Thr Thr Gln Leu Val Leu Lys Asn Arg Gly
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133 gtg tat gag agc gtg aag tac atc cag cag gag aac ttc tgg att ggc    1296
134 Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly
135             420             425             430
137 ccc agc tcg att gac ctc att cac ctg gga gca aag ttc tcg ccc tgc    1344
138 Pro Ser Ser Ile Asp Leu Ile His Leu Gly Ala Lys Phe Ser Pro Cys
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141 atc cgg aag gac cag caa att gag cag ctg gta cgg agg gag cgc gac    1392
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145 att gag cgc acc tct ggc tgc tgt gtc cag aat gac cgc tcg ggc tgc    1440
146 Ile Glu Arg Thr Ser Gly Cys Cys Val Gln Asn Asp Arg Ser Gly Cys
147 465             470             475             480
149 atc cag acc ctg aag aag gac tgc tcg gag act tta gcc acg ttc gta    1488
150 Ile Gln Thr Leu Lys Lys Asp Cys Ser Glu Thr Leu Ala Thr Phe Val
151             485             490             495
153 aag tgg cag aat gat act ggg ccc tca gac aag tct gac ctg agc cag    1536
154 Lys Trp Gln Asn Asp Thr Gly Pro Ser Asp Lys Ser Asp Leu Ser Gln
155             500             505             510
157 aag cag cca tcg gcg gtt gtg tgc cac caa gac ccc agg acc tgt gaa    1584
158 Lys Gln Pro Ser Ala Val Val Cys His Gln Asp Pro Arg Thr Cys Glu
159             515             520             525
161 gag cct gcc tcc agt ggg gcc cac atc tgg cct gat gac att acc aag    1632
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165 tgg ccg atc tgc aca gag cag gct cag agc aac cac acg ggc ttg ttg    1680
166 Trp Pro Ile Cys Thr Glu Gln Ala Gln Ser Asn His Thr Gly Leu Leu
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169 cac ata gac tgt aag atc aaa ggc cgc ccc tgc tgc atc ggc acc aag    1728
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173 ggc agc tgc gag atc acc act cgg gag tac tgt gag ttc atg cat ggc    1776
174 Gly Ser Cys Glu Ile Thr Thr Arg Glu Tyr Cys Glu Phe Met His Gly
175             580             585             590
177 tat ttc cat gaa gac gcg acg ctg tgt tcc cag gtg cac tgt tta gac    1824
178 Tyr Phe His Glu Asp Ala Thr Leu Cys Ser Gln Val His Cys Leu Asp
179             595             600             605
181 aag gtg tgt ggg ctc ctg cct ttc ctc aac cct gag gtc cct gac cag    1872
182 Lys Val Cys Gly Leu Leu Pro Phe Leu Asn Pro Glu Val Pro Asp Gln
183     610             615             620
185 ttc tac cgg atc tgg ctg tct tta ttc ctg cat gct ggc ata gtg cac    1920
186 Phe Tyr Arg Ile Trp Leu Ser Leu Phe Leu His Ala Gly Ile Val His
187 625             630             635             640
189 tgc ctt gtg tct gtg gtc ttc caa atg acc atc ctg agg gac cta gag    1968
190 Cys Leu Val Ser Val Val Phe Gln Met Thr Ile Leu Arg Asp Leu Glu
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195                  660                  665                  670
197 att aca ggc aac ctg gcc agc gcc atc ttc ctc ccc tac cgg gca gag     2064
198 Ile Thr Gly Asn Leu Ala Ser Ala Ile Phe Leu Pro Tyr Arg Ala Glu
199         675                  680                  685
201 gtg ggc cca gcc ggg tcg cag ttc ggc ctc ctc gcc tgc ctc ttc gtg     2112
202 Val Gly Pro Ala Gly Ser Gln Phe Gly Leu Leu Ala Cys Leu Phe Val
203         690                  695                  700
205 gag ctg ttc cag agc tgg cag ctg ttg gag cgg ccg tgg aag gcc ttc     2160
206 Glu Leu Phe Gln Ser Trp Gln Leu Leu Glu Arg Pro Trp Lys Ala Phe
207 705                  710                  715                  720
209 ttc aac ctg tcg gcc att gtg ctt ttc ctc ttc atc tgt ggc ctc ctg     2208
210 Phe Asn Leu Ser Ala Ile Val Leu Phe Leu Phe Ile Cys Gly Leu Leu
211                  725                  730                  735
213 ccc tgg ata gac aac atc gcc cac atc ttc ggg ttc ctc agc ggc atg     2256
214 Pro Trp Ile Asp Asn Ile Ala His Ile Phe Gly Phe Leu Ser Gly Met
215                  740                  745                  750
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218 Leu Leu Ala Phe Ala Phe Leu Pro Tyr Ile Thr Phe Gly Thr Ser Asp
219         755                  760                  765
221 aag tac cgc aag cga gcc ctc atc ctc gtg tcg ctg ctg gtc ttt gct     2352
222 Lys Tyr Arg Lys Arg Ala Leu Ile Leu Val Ser Leu Leu Val Phe Ala
223         770                  775                  780
225 ggg ctc ttt gct tcc ctg gtg ctg tgg ctg tac atc tac ccc atc aac     2400
226 Gly Leu Phe Ala Ser Leu Val Leu Trp Leu Tyr Ile Tyr Pro Ile Asn
227 785                  790                  795                  800
229 tgg ccc tgg atc gag tac ctc acc tgc ttt ccc ttc acc agc cgc ttc     2448
230 Trp Pro Trp Ile Glu Tyr Leu Thr Cys Phe Pro Phe Thr Ser Arg Phe
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250         20                  25                  30
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254         35                  40                  45
257 Arg Arg Lys Asn Pro Ala Tyr Leu Lys Ser Val Ser Leu Gln Glu Pro
258 50                  55                  60
261 Arg Gly Arg Trp Gln Glu Gly Ala Glu Lys Arg Pro Gly Phe Arg Arg
262 65                  70                  75                  80
```

```
265 Gln Ala Ser Leu Ser Gln Ser Ile Arg Lys Ser Thr Ala Gln Trp Phe
266             85                  90              95
269 Gly Val Ser Gly Asp Trp Glu Gly Lys Arg Gln Asn Trp His Arg Arg
270             100                 105             110
273 Ser Leu His His Cys Ser Val His Tyr Gly Arg Leu Lys Ala Ser Cys
274         115             120             125
277 Gln Arg Glu Leu Glu Leu Pro Ser Gln Glu Val Pro Ser Phe Gln Gly
278     130             135             140
281 Thr Glu Ser Pro Lys Pro Cys Lys Met Pro Lys Ile Val Asp Pro Leu
282 145             150             155                 160
285 Ala Arg Gly Arg Ala Phe Arg His Pro Asp Glu Val Asp Arg Pro His
286             165             170             175
289 Ala Ala His Pro Pro Leu Thr Pro Gly Val Leu Ser Leu Thr Ser Phe
290             180             185             190
293 Thr Ser Val Arg Ser Gly Tyr Ser His Leu Pro Arg Arg Lys Arg Ile
294         195             200             205
297 Ser Val Ala His Met Ser Phe Gln Ala Ala Ala Leu Leu Lys Gly
298         210             215             220
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302 225             230             235                 240
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346             405             410             415
349 Val Tyr Glu Ser Val Lys Tyr Ile Gln Gln Glu Asn Phe Trp Ile Gly
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VERIFICATION SUMMARY   DATE: 05/25/2005
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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:25